

# ENTERED



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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/057,288

DATE: 02/15/2002

TIME: 14:09:29

Input Set : A:\D0136np1.app

Output Set: N:\CRF3\02152002\J057288.raw

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3 <110> APPLICANT: Larsen, Christian P.
4     Pearson, Thomas C.
5     Waller, Edmund K.
6     Adams, Andrew B.
8 <120> TITLE OF INVENTION: METHODS OF INDUCING ORGAN TRANSPLANT TOLERANCE AND
9     CORRECTING HEMOGLOBINOPATHIES
11 <130> FILE REFERENCE: D0136NP/30436.58USU1
C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/057,288
14 <141> CURRENT FILING DATE: 2002-01-25
16 <150> PRIOR APPLICATION NUMBER: 60/264,528
17 <151> PRIOR FILING DATE: 2001-01-26
19 <150> PRIOR APPLICATION NUMBER: 60/303,142
20 <151> PRIOR FILING DATE: 2001-07-05
22 <160> NUMBER OF SEQ ID NOS: 20
24 <170> SOFTWARE: PatentIn Ver. 2.1
26 <210> SEQ ID NO: 1
27 <211> LENGTH: 1152
28 <212> TYPE: DNA
29 <213> ORGANISM: Artificial Sequence
31 <220> FEATURE:
32 <223> OTHER INFORMATION: Description of Artificial Sequence: L104EIg
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38 ggcacgcta gctttgtgtg tgagtatgca tctccaggca aagccactga ggtccgggtg 180
39 acagtgttc ggcaggctga cagccagggtg actgaagtct gtgcggcaac ctacatgatg 240
40 gggaatgagt tgaccttcct agatgattcc atctgcacgg gcacctccag tggaaatcaa 300
41 gtgaacctca ctatccaagg actgagggcc atggacacgg gactctacat ctgcaagggtg 360
42 gagctcatgt acccaccgcc atactacgag ggcataggca acggaaccca gatttatgta 420
43 attgatccag aaccgtgccc agattctgat caggagccca aatcttctga caaaactcac 480
44 acatccccac cgtccccagc acctgaactc ctggggggat cgtcagtcct cctcttcccc 540
45 ccaaaaccca aggacaccct catgatctcc cggacccttg aggtcacatg cgtggtggtg 600
46 gacgtgagcc acgaagaccc tgaggtcaag ttcaactggt acgtggacgg cgtggagggtg 660
47 cataatgcca agacaaagcc gcgggaggag cagtacaaca gcacgtaccg tgtggtcagc 720
48 gtctcaccg tcctgcacca ggactggctg aatggcaagg agtacaagtg caaggctctcc 780
49 aacaaagccc tcccagcccc catcgagaaa accatctcca aagccaaagg gcagccccga 840
50 gaaccacagg tgtacaccct gccccatcc cgggatgagc tgaccaagaa ccaggtcagc 900
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52 gggcagccgg agaacaacta caagaccacg cctcccgtgc tggactccga cggctccttc 1020
53 ttctctaca gcaagctcac cgtggacaag agcagggtggc agcaggggaa cgtcttctca 1080
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58 <210> SEQ ID NO: 2
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65     sequence
67 <400> SEQUENCE: 2
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71 Leu Leu Phe Pro Ser Met Ala Ser Met Ala Met His Val Ala Gln Pro
72           20           25           30
74 Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu
75           35           40           45
77 Tyr Ala Ser Pro Gly Lys Ala Thr Glu Val Arg Val Thr Val Leu Arg
78           50           55           60
80 Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala Ala Thr Tyr Met Met
81 65           70           75           80
83 Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser
84           85           90           95
86 Ser Gly Asn Gln Val Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp
87           100          105          110
89 Thr Gly Leu Tyr Ile Cys Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr
90           115          120          125
92 Tyr Glu Gly Ile Gly Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu
93           130          135          140
95 Pro Cys Pro Asp Ser Asp Gln Glu Pro Lys Ser Ser Asp Lys Thr His
96 145          150          155          160
98 Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu Leu Gly Gly Ser Ser Val
99           165          170          175
101 Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
102           180          185          190
104 Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
105           195          200          205
107 Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
108           210          215          220
110 Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
111 225          230          235          240
113 Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
114           245          250          255
116 Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
117           260          265          270
119 Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
120           275          280          285
122 Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
123           290          295          300
125 Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
126 305          310          315          320
128 Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser

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129          325          330          335
131 Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
132          340          345          350
134 Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
135          355          360          365
137 His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
138          370          375          380
141 <210> SEQ ID NO: 3
142 <211> LENGTH: 1152
143 <212> TYPE: DNA
144 <213> ORGANISM: Artificial Sequence
146 <220> FEATURE:
147 <223> OTHER INFORMATION: Description of Artificial Sequence: L104EA29YIg
148 sequence
150 <400> SEQUENCE: 3
151 atgggtgtac tgctcacaca gaggacgctg ctcagtctgg tccttgcaact cctgtttcca 60
152 agcatggcga gcatggcaat gcacgtggcc cagcctgctg tggactaggc cagcagccga 120
153 ggcacgcgta gctttgtgtg tgagtatgca tctccaggca aatatactga ggtccgggtg 180
154 acagtgtctc ggcaggctga cagccagggt actgaagtct gtgcggcaac ctacatgatg 240
155 gggaatgagt tgaccttcct agatgattcc atctgcacgg gcacctccag tggaaatcaa 300
156 gtgaacctca ctatccaagg actgagggcc atggacacgg gactctacat ctgcaagggtg 360
157 gagctcatgt acccaccgcc atactacgag ggcataggca acggaacca gatttatgta 420
158 attgatccag aaccgtgccc agattctgat caggagccca aatcttctga caaaactcac 480
159 acatccccac cgtccccagc acctgaactc ctggggggat cgtcagtcct cctcttcccc 540
160 caaaaacca aggacaccct catgatctcc cggaccctg aggtcacatg cgtggtggtg 600
161 gacgtgagcc acgaagaccc tgaggtcaag ttcaactggt acgtggacgg cgtggagggtg 660
162 cataatgcca agacaaagcc gcgggaggag cagtacaaca gcacgtaccg tgtggtcagc 720
163 gtctcaccg tcctgcacca ggactggctg aatggcaagg agtacaagtg caaggctctc 780
164 aacaaagccc tcccagcccc catcgagaaa accatctcca aagccaaagg gcagccccga 840
165 gaaccacagg tgtacaccct gcccccatcc cgggatgagc tgaccaagaa ccaggtcagc 900
166 ctgacctgcc tggtaaagg cttctatccc agcgacatcg ccgtggagtg ggagagcaat 960
167 gggcagccgg agaacaacta caagaccag cctcccgctg tggactccga cggctccttc 1020
168 ttctcttaca gcaagctcac cgtggacaag agcagggtggc agcaggggaa cgtcttctca 1080
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170 ccgggtaaat ga 1152
173 <210> SEQ ID NO: 4
174 <211> LENGTH: 383
175 <212> TYPE: PRT
176 <213> ORGANISM: Artificial Sequence
178 <220> FEATURE:
179 <223> OTHER INFORMATION: Description of Artificial Sequence: L104EA29YIg
180 sequence
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184 1 5 10 15
186 Leu Leu Phe Pro Ser Met Ala Ser Met Ala Met His Val Ala Gln Pro
187 20 25 30
189 Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu
190 35 40 45

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192 Tyr Ala Ser Pro Gly Lys Tyr Thr Glu Val Arg Val Thr Val Leu Arg
193      50                      55                      60
195 Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala Ala Thr Tyr Met Met
196 65      70                      75                      80
198 Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser
199      85                      90                      95
201 Ser Gly Asn Gln Val Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp
202      100                     105                     110
204 Thr Gly Leu Tyr Ile Cys Lys Val Glu Leu Met Tyr Pro Pro Tyr
205      115                     120                     125
207 Tyr Glu Gly Ile Gly Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu
208      130                     135                     140
210 Pro Cys Pro Asp Ser Asp Gln Glu Pro Lys Ser Ser Asp Lys Thr His
211 145                     150                     155                     160
213 Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu Leu Gly Gly Ser Ser Val
214      165                     170                     175
216 Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
217      180                     185                     190
219 Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
220      195                     200                     205
222 Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
223      210                     215                     220
225 Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
226 225                     230                     235                     240
228 Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
229      245                     250                     255
231 Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
232      260                     265                     270
234 Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
235      275                     280                     285
237 Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
238      290                     295                     300
240 Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
241 305                     310                     315                     320
243 Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
244      325                     330                     335
246 Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
247      340                     345                     350
249 Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
250      355                     360                     365
252 His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
253      370                     375                     380
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257 <211> LENGTH: 1152
258 <212> TYPE: DNA
259 <213> ORGANISM: Artificial Sequence
261 <220> FEATURE:
262 <223> OTHER INFORMATION: Description of Artificial Sequence: L104EA29LIg
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265 &lt;400&gt; SEQUENCE: 5

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266 atgggtgtac tgctcacaca gaggacgctg ctcagtctgg tccttgcaact cctgtttcca 60
267 agcatggcga gcatggcaat gcacgtggcc cagcctgctg tggtagctggc cagcagccga 120
268 ggcatcgcta gctttgtgtg tgagtatgca tctccaggca aattgactga ggtccgggtg 180
269 acagtgcctt ggcaaggctga cagccagggtg actgaagtct gtgcggcaac ctacatgatg 240
270 gggaatgagt tgaccttcct agatgattcc atctgcacgg gcacctccag tggaaatcaa 300
271 gtgaacctca ctatccaagg actgagggcc atggacacgg gactctacat ctgcaagggtg 360
272 gagctcatgt acccaccgcc atactacgag ggcataggca acggaacca gatttatgta 420
273 attgatccag aaccgtgccc agattctgat caggagccca aatcttctga caaaactcac 480
274 acatccccac cgtccccagc acctgaactc ctggggggat cgtcagtctt cctcttcccc 540
275 ccaaaaccca aggacacct catgatctcc cggacccttg aggtcacatg cgtgggtggtg 600
276 gacgtgagcc acgaagacc tgaggtcaag ttcaactggt acgtggacgg cgtggaggtg 660
277 cataatgcc aagacaaagg gcgggaggag cagtacaaca gcacgtaccg tgtggtcagc 720
278 gtctctaccg tctgcacca ggactggctg aatggcaagg agtacaagtg caaggtctcc 780
279 aacaaagccc tcccagcccc catcgagaaa accatctcca aagccaaagg gcagccccga 840
280 gaaccacagg tgtacacctt gccccatcc cgggatgagc tgaccaagaa ccaggtcagc 900
281 ctgacctgcc tgggtcaaagg cttctatccc agcgacatcg ccgtggagtg ggagagcaat 960
282 gggcagccgg agaacaacta caagaccacg cctcccgctg tggactccga cggctccttc 1020
283 ttctctaca gcaagctcac cgtggacaag agcagggtggc agcaggggaa cgtcttctca 1080
284 tgctccgtga tgcattgagg tctgcaacaac cactacacgc agaagagcct ctccctgtct 1140
285 ccgggtaaat ga 1152

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289 &lt;211&gt; LENGTH: 383

290 &lt;212&gt; TYPE: PRT

291 &lt;213&gt; ORGANISM: Artificial Sequence

293 &lt;220&gt; FEATURE:

294 <223> OTHER INFORMATION: Description of Artificial Sequence: L104EA29LIg  
 295 sequence

297 &lt;400&gt; SEQUENCE: 6

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301 Leu Leu Phe Pro Ser Met Ala Ser Met Ala Met His Val Ala Gln Pro
302           20           25           30
304 Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu
305           35           40           45
307 Tyr Ala Ser Pro Gly Lys Leu Thr Glu Val Arg Val Thr Val Leu Arg
308           50           55           60
310 Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala Ala Thr Tyr Met Met
311           65           70           75           80
313 Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser
314           85           90           95
316 Ser Gly Asn Gln Val Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp
317           100          105          110
319 Thr Gly Leu Tyr Ile Cys Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr
320           115          120          125
322 Tyr Glu Gly Ile Gly Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu
323           130          135          140
325 Pro Cys Pro Asp Ser Asp Gln Glu Pro Lys Ser Ser Asp Lys Thr His
326 145          150          155          160

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VERIFICATION SUMMARY

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L:13 M:270 C: Current Application Number differs, Replaced Current Application Number